



SEQUENCE LISTING

#8

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<110> Lerner, Richard A
Sorge, Joseph A
Winter, Gregory P
Riechman, Lutz

<120> A new method for tapping the immunological repertoire

<130> 213839-00023

<140> 09/726,649

<141> 2000-11-28

<160> 121

<170> PatentIn version 3.1

<210> 1

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe

20

25

30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Asp Tyr Pro His Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Phe
 85 90 95

Tyr Cys Ala Arg Asp Phe Tyr Arg Tyr Asp Gly
 100 105

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Phe Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Arg Tyr Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Leu Ser Gly Phe Leu Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Arg Asn Lys Val Tyr Asp Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asp Ala Tyr Tyr Gly Ser Tyr Trp Tyr Phe Asp Val
100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Ala Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Phe Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Val Tyr Tyr Gly Tyr Asp Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Ile Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Ser Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asp
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<222> (1)..(88)
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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Ile Thr Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu
85

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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 <223> Y5236-myeloma protein

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

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<222> (1)..(123)
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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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<220>
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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Asn Tyr Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Arg Asn Lys Gly Asn Lys Tyr Thr Thr Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Trp Tyr Phe Asp Val
100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 17
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<223> W3207-myeloma protein

<400> 17

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Phe Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Lys Tyr Asp Leu Trp Tyr Val Asp Val
 100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 115 120

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 <212> PRT
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<220>
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 <223> M511-myeloma protein

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
 20 25 30

Tyr Met Glu Trp Val Arg Gln Ser Pro Gly Lys Arg Leu Glu Trp Ile
 35 40 45

Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
 50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
85 90 95

Tyr Cys Ala Arg Asp Gly Asp Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp
100 105 110

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

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<223> M167-myeloma

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Glu Val Val Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30

Tyr Met Glu Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Ile
35 40 45

Ala Ala Ser Arg Ser Lys Ala His Asp Tyr Thr Arg Glu Tyr Ser Ala
50 55 60

Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Val
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Thr Tyr
85 90 95

Tyr Cys Thr Arg Asp Ala Asp Tyr Gly Asn Ser Tyr Phe Gly Tyr Phe
100 105 110

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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actggctact ccataccag tgcttattac tggaactgga tccggcagtt 110

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<212> DNA
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<223> n=A,T,C, or G

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tctggccaca ccttgactag ttactggata cactgggtaa aanagaggcc 110

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<223> n=A, T, C or G

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<223> n=A, T, C or G

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ctggatacac attcacnagc tatgttatac actgggtgaa gcagaagcct 110

<210> 23
<211> 110
<212> DNA
<213> Mus musculus

<400> 23
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tctggataca cattcaccag ctatgttatg cgctgggtga agcagaagcc 110

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<223> n=A, T, C or G

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<211> 110
<212> DNA
<213> Mus musculus

<220>
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<223> n=A, T, C or G

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tctggctact ccttcacnag ctactggatg aactgggtga agcagaggcc 110

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<223> n= A, T, C or G

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tctcgctact cttcaccagc tcttgataac tgggtgaagc agaggcctgg 110

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<210> 28
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tcaggattcg atttnagnag ataatggatg agttgggttc ggcaggctcc 110

<210> 29
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<223> n=A, T, C or G

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tcaggattcg atttnagnag atactggatg agttgggtcc ggcagctcca 110

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<220>
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<222> (1)..(110)
<223> n=A, T, C or G

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tcaggattcg atttnagnag atactggatg agttgggtcc gcagctccag 110

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<223> n=A, T, C or G

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<220>
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<222> (1)..(110)
<223> n=A, T, C or G

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tcaggctatt ccttcaccag ctactggatg cactgggtga aacagaggcc 110

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<211> 172
<212> DNA
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<220>
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ctagactagt taccggtacg acgttcgga ctacggttct taatagaatt cg 172

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<211> 136
<212> DNA
<213> Unknown

<220>
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ctagactagt taatag 136

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<220>
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ccgctggatt gttattactc gctgcccac cagccatggc cgagctcgtc agttctagag 120
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<220>
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 ccgctggatt gttattactc gctgccaac cagccatggc cgagctcgtc agttctagag 120

 ttaagcggcc g 131

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 aggtccagct gctcgagtct gg 22

<210> 43
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 <213> Unknown

<220>
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 <400> 43
 aggtccagct gctcgagtca gg 22

<210> 44
 <211> 22
 <212> DNA
 <213> Unknown

<220>
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 <400> 44
 aggtccagct tctcgagtct gg 22

<210> 45
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<220>
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 <400> 45

aggtccagct tctcgagtca gg 22

<210> 46
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<220>
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<400> 46
aggtccaact gctcgagtct gg 22

<210> 47
<211> 22
<212> DNA
<213> Unknown

<220>
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<400> 47
aggtccaact gctcgagtca gg 22

<210> 48
<211> 22
<212> DNA
<213> Unknown

<220>
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<400> 48
aggtccaact tctcgagtct gg 22

<210> 49
<211> 22
<212> DNA
<213> Unknown

<220>
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<400> 49
aggtccaact tctcgagtca gg 22

<210> 50
<211> 20
<212> DNA
<213> Unknown

<220>

<223> 5' degenerate primer containing inosine at 4 degenerate positions

<220>

<221> misc_feature

<222> (1)..(20)

<223> n=inosine

<400> 50

aggtnnanct nctcgagtct

20

<210> 51

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(20)

<223> n=inosine

<400> 51

aggtnnanct nctcgagtca

20

<210> 52

<211> 19

<212> DNA

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<223> Synthetic

<400> 52

gcccaaggat gtgctcacc

19

<210> 53

<211> 39

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 53

ctattagaat tcaacggtaa cagtgggtgcc ttggcccca

39

<210> 54

<211> 39

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 54

ctattaacta gtaacggtaa cagtgggtgcc ttggcccca

39

<210> 55

<211> 19

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 55

ctcagtatgg tggttgtgc

19

<210> 56

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 56

gctactagtt ttgatttcca ccttgg

26

<210> 57

<211> 23

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 57

cagccatggc cgacatccag atg

23

<210> 58

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 58

aattttacta gtcaccttgg tgctgctggc

30

<210> 59
<211> 39
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 59
tatgcaacta gtacaaccac aatccctggg cacaatttt

39

<210> 60
<211> 32
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 60
ccagttccga gctcgttggtg actcaggaat ct

32

<210> 61
<211> 32
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 61
ccagttccga gctcgtgttg acgcagccgc cc

32

<210> 62
<211> 32
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 62
ccagttccga gctcgtgctc acccagtcctc ca

32

<210> 63
<211> 32
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 63

ccagttccga gctccagatg acccagtctc ca 32

<210> 64

<211> 32

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 64

ccagatgtga gctcgtgatg acccagactc ca 32

<210> 65

<211> 32

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 65

ccagatgtga gctcgtcatg acccagtctc ca 32

<210> 66

<211> 32

<212> DNA

<213> Unknown

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<400> 66

ccagatgtga gctcgtgata acccaggatg aa 32

<210> 67

<211> 32

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<400> 67

gcagcattct agagtttcag ctccagcttg cc 32

<210> 68

<211> 33

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 68

ccgccgtcta gaacactcat tctgttgaa gct

33

<210> 69

<211> 33

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 69

ccgccgtcta gaacattctg caggagacag act

33

<210> 70

<211> 32

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 70

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32

<210> 71

<211> 34

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 71

gcgccgtcta gaattaacac tcattcctgt tgaa

34

<210> 72

<211> 38

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 72

ctattaacta gtaacggtaa cagtgggtgcc ttgcccc

38

<210> 73

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 73

aggcttacta gtacaatccc tgggcacaat

30

<210> 74

<211> 29

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 74

gccgctctag aacactcatt cctgttgaa

29

<210> 75

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(22)

<223> n=inosine

<400> 75

aggtnnanct nctcgagtct gc

22

<210> 76

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(22)

<223> n=inosine

<400> 76

aggtnnanct nctcgagtca gc

22

<210> 77
<211> 35
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 77
gtgccagatg tgagctcgtg atgacccagt ctcca' 35

<210> 78
<211> 34
<212> DNA
<213> Unknown

<220>
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<400> 78
tccttctaga ttactaacac tctcccctgt tgaa 34

<210> 79
<211> 31
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 79
gcattctaga ctattaacat tctgtagggg c 31

<210> 80
<211> 37
<212> DNA
<213> Unknown

<220>
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<400> 80
ctgcacaggg tcctgggccg agctcgtggt gactcag 37

<210> 81
<211> 22
<212> DNA
<213> Unknown

<220>
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<220>

<221> misc_feature
<222> (1)..(22)
<223> n=inosine

<400> 81
agntgcannt gctcgagtct gg 22

<210> 82
<211> 43
<212> DNA
<213> Unknown

<220>
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<400> 82
gtgggcatgt gtgagttgtg tcactagttg gggttttgag etc 43

<210> 83
<211> 30
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 83
cggactagta caagatttgg gctctgcttt 30

<210> 84
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(22)
<223> s=C or G, m= C or A, r= G or T, k= G or T, w= T or A

<400> 84
aggtsmarct kctcgagtcw gg 22

<210> 85
<211> 32
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 85

ggccgcgcaaat tctattttcaa ggagacagtc at

32

<210> 86

<211> 36

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 86

aatgaaatac ctattgccta cggcagccgc tggatt

36

<210> 87

<211> 31

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 87

gttattactc gctgcccaac cagccatggc c

31

<210> 88

<211> 38

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 88

aggtgaaact gctcgagaat tctagactag gttaatag

38

<210> 89

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 89

tcgactatta actagtctag aattctcgag

30

<210> 90

<211> 29

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 90

cagtttcacc tgggcātgg ctggttggg

29

<210> 91

<211> 40

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 91

cagcgagtaa taacaatcca gcggctgccg taggcaatag

40

<210> 92

<211> 38

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 92

gtatttcatt atgactgtct ccttgaaata gaatttgc

38

<210> 93

<211> 40

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 93

aggtgaaact gctcgagatt tctagactag ttaccggtac

40

<210> 94

<211> 33

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 94

gacgttcggg actacggttc ttaatagaat tcg

33

<210> 95
<211> 28
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 95
tcgacgaatt ctattaagaa ccgtagtc 28

<210> 96
<211> 38
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 96
cggaacgtcg tacgggtaac tagtctagaa atctcgag 38

<210> 97
<211> 34
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 97
tgaattctaa actagtcgcc aaggagacag tcac 34

<210> 98
<211> 30
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 98
gagctcgtca gttctagagt taagcggccg 30

<210> 99
<211> 48
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 99

gtatttcatt atgactgtct ccttggcgac tagtttagaa ttcaagct 48

<210> 100

<211> 40

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 100

cagcgagtaa taacaatcca gcggctgccg taggcaatag 40

<210> 101

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 101

tgacgagctc ggccatggct ggttggg 27

<210> 102

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 102

tcgacggccg cttaactcta gaac 24

<210> 103

<211> 28

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 103

aataagcttg atctatcagt aatcgacc 28

<210> 104

<211> 31

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 104

attagatctg aattctgacg tccgttatca g

31

-<210> -105-

<211> 56

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 105

gatccgcttc ccgataaggg agcaggccag taaaagcatt acctgtggtg gggttc

56

<210> 106

<211> 51

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 106

ccgagcggcc aaaggagca gactctaaat ctgccgtcat cgacttcgaa g

51

<210> 107

<211> 42

<212> DNA

<213> Unknown

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<400> 107

gttcgaatcc ttccccacc accatcactt tcaaaagtcc ga

42

<210> 108

<211> 56

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 108

ctagtcggac ttttgaaagt gatggtggtg ggggaaggat tcgaaccttc gaagtc

56

<210> 109

<211> 52

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(52)

<223> r= G or A

<400> 109

gatgacggca gatttagagt ctgctccctr ttggccgctc gggaaccca cc

52

<210> 110

<211> 42

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 110

acaggtaatg cttttactgg cctgctccct tatcggaag cg

42

<210> 111

<211> 9

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 111

tcgagcgcc

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<210> 112

<211> 9

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<400> 112

gatcggcgc

9

<210> 113

<211> 9

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 113
ctagggcct

9

<210> 114

<211> 9

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 114
ctagaggcc

9

<210> 115

<211> 5

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 115
cgccc

5

<210> 116

<211> 13

<212> DNA

<213> Unknown

<220>

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<400> 116
gatcgggcga gct

13

<210> 117

<211> 41

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 117
ctagttaccc gtacgacgtt ccggactacg cttcttaata g

41

<210> 118

<211> 40

<212> DNA

<213> Unknown

<220>

<223> Synthetic

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aattctatta agaagcgtag tccggāacgt cgacgggtaa

40

<210> 119

<211> 199

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 119

tcgagcgccg atccgcttcc cgataaggga gcaggccagt aaaagcatta cctgtggtgg 60

ggttcccag cgccaaagg gagcagactc taaatctgcc gtcattcgact tcgaagggtc 120

gaatccttcc cccaccacca tcactttcaa aagtccgact agttaccggt acgacgttcc 180

ggactacgct tcttaatag 199

<210> 120

<211> 162

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 120

cgccccgatcc gcttcccgat aaggaggagcag gccagtaaaa gcattacctg tgggtggggtt 60

cccagcggcc aaaggagca gactctaaat ctgccgtcat cgacttcgaa gggttcgaatc 120

cttccccac caccatcact ttcaaaagtc cgactagggc ct 162

<210> 121

<211> 32

<212> DNA

<213> Unknown

<220>

<223> Synthetic

<400> 121

ccagatgtga gctcgtgata acccaggatg aa

32

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